

Gene Section

Review

KLK7 (kallikrein-related peptidase 7)

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Identity

Other names: PRSS6; SCCE; hK7; hSCCE

HGNC (Hugo): KLK7

Location: 19q13.33

Local order: Telomere to centromere.

DNA/RNA

Description

The gene encompasses 6.509 kb of gDNA.

Transcription

Five variant mRNA transcripts have been identified. These include transcripts using different 5' untranslated regions (UTRs) including exon 1 deletions, and transcripts using different 3'UTR regions. Using rapid amplification of cDNA ends (RACE) different KLK7 5'UTR sequences were identified from RNA extracted from pancreas, skin

and ovarian cells, suggesting the expression of tissue specific KLK7 transcripts.

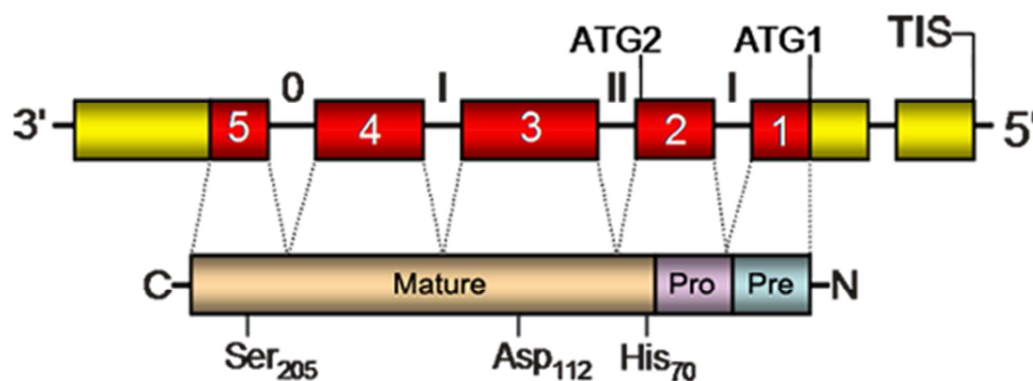
Pseudogene

Not identified.

Protein

Description

Full-length KLK7 (253 amino acids) has a secretion signal (pre-) peptide (22 amino acids), followed by an activation (pro-) peptide (7 amino acids) and the mature chain (224 amino acids) with 1 potential N-linked glycosylation site. The catalytic triad of His₇₀, Asp₁₁₂ and Ser₂₀₅ (relative to ATG1) is conserved and is essential for proteolytic activity. After synthesis as a KLK7 full-length protein, the signal peptide is then cleaved and pro-KLK7 (zymogen) is subsequently secreted from the cell. On activation, the propeptide is removed and the zymogen becomes the mature active enzyme.



Genomic and protein structure of the KLK7 gene. The KLK7 gene is classically comprised of 5 coding exons (red boxes, classic numerals) and 4 intervening introns with a conserved intron phase pattern (I, II, I, 0). A non-coding exon and untranslated regions are shown in yellow. Also shown is the classical transcription initiation site (TIS) and corresponding translation start site (ATG1). An exon 1 deleted transcript has also been identified which would potentially result in the use of an alternative translation start site (ATG2). The numbering for the amino acid residues of the catalytic triad (His₇₀, Asp₁₁₂, Ser₂₀₅) are relative to the full-length protein starting from ATG1.

KLK7 can complex with antileukoprotease (secretory leukocyte protease inhibitor), elafin, Lympho-epithelial Kazal type inhibitor (LEKTI) fragments, and a member of α 2-macroglobulin (α 2M) protease inhibitor family, α 2-macroglobulin-like 1 (α 2ML1).

X-ray structures of recombinant full-length KLK7 from *E. coli* and insect cells have been solved, from which the most distinguishing features of KLK7 are the short 70-80 loop and the unique S1 pocket, which prefers P1 Tyr residues. KLK7 displays a unique chymotrypsin-like specificity for Tyr, which is preferred at P2. In addition, KLK7 exhibits large positively charged surface patches, representing putative exosites for prime side substrate recognition.

Similar to several other KLKs and based on the binding of metal to histidine such as His₉₉, the KLK7 activity is inhibited by Zn⁺⁺ and Cu⁺⁺ at low micromolar concentrations. KLK7 induced degradation of corneodesmosin and desmocollin 1 with similar efficiency in acidic (pH 5.6) and neutral (pH 7.2) conditions. KLK7 activity is modulated by water content in stratum corneum as KLK7 activity increased significantly in an environment of high relative humidity. KLK7 also demonstrated a tolerance to water restriction suggesting that it may be adapted to function in the water-restricted stratum corneum. Thus, relative humidity modulates desquamation by its effect upon KLK7 activity, possibly other desquamatory hydrolases and adapted KLK7 function in water-deplete skin.

An N-terminal truncated KLK7 isoform (181 amino acids) initiating from the putative ATG2 would not have the pre-pro-region and 43 amino acids from the N-terminus of full-length KLK7. The histidine which is part of the catalytic triad is also omitted which would result in a proteolytic inactive protein. The presence of this isoform has not yet been confirmed in human tissues or biological fluids.

Expression

Full-length KLK7 protein was originally purified in human skin and named stratum corneum chymotryptic enzyme (SCCE, hSCCE). KLK7 cDNA was originally isolated from a keratinocyte derived library and designated PRSS6. Although Northern blot analyses have shown that KLK7 mRNA is predominantly localised to skin and pancreas, more sensitive RT-PCR experiments have shown that brain, kidney, ovary, bone, breast, endometrium, spinal cord, lung, prostate tissue and salivary tissue express KLK7 mRNA at low to modest levels. High KLK7 mRNA has been detected in malignancies of ovary, breast, lung and brain.

KLK7 protein has been detected by ELISA in a wide range of tissues at low (adrenal, bladder, cervix, fallopian tube, kidney, lung, lymph node, muscle, ovary, salivary gland, small intestine, spinal cord, spleen, thyroid gland, tonsil, trachea and vagina) to high (oesophagus, heart, liver and skin) levels. Modest levels of KLK7 protein have also been detected in

human body fluid, such as, seminal plasma, breast milk, ovarian cancer ascites, salivary and cervicovaginal fluid.

In normal skin, KLK7 is expressed in late epidermal differentiation and found at all sites of epithelial cornification. Consequently, KLK7 is used as a marker for terminal epidermal differentiation. In normal epidermis, KLK7 was detected in a population of dendritic cells and in high suprabasal keratinocytes. KLK7 was also found in reconstructed human epidermis and its expression was suppressed by retinoic acid. An increased expression of KLK7 was found in suprabasal cells in orthokeratotic and parakeratotic areas of the lesions of oral lichen planus (an inflammatory disease) and benign oral keratosis (a non-inflammatory disease).

High KLK7 protein levels have been detected in the tissues of lung, breast, ovarian and squamous cervical cancers, oral squamous cell carcinoma and cervical adenocarcinoma tissues from patients. However, KLK7 is down regulated in cancerous prostate tissues compared to normal prostate tissues. KLK7, along with KLK6 and KLK10, is decreased in cerebrospinal fluid of frontotemporal dementia patients.

Localisation

Full-length KLK7 is localised intracellularly in the cytoplasm prior to secretion. KLK7 protein is co-localised with KLK5 in skin and acinar cells of the pancreas by immunohistochemical staining.

The putative N-terminal truncated KLK7-181 isoform is potentially not secreted as it does not have a signal peptide, and cellular localisation remains to be determined.

Function

To date, the major biological functions of KLK7 are associated with the skin and related epithelial tissues, such as hair follicles, oral mucosa and glandular lobules. KLK7 is involved in keratinization, stratum corneum formation, and turnover/ desquamation of the skin through the degradation of cell adhesion glycoproteins, such as corneodesmosin, desmocollin 1 and plakoglobin. KLK7 has also been shown to cleave insulin B chain, degrade fibronectin, fibrinogen and interleukin 1beta (IL-1b), as well as activate pro-IL-1b. KLK7 and KLK5 can control activation of the human cathelicidin precursor protein, hCAP18, implying their ability to control innate immune defence.

An in vitro study showed that UVB radiation can increase KLK7 and KLK5 expression at both mRNA and protein levels in keratinocyte (HaCat) cells. In the epidermis, the major inhibitor of KLK7, antileukoprotease (secretory leukocyte protease inhibitor) is produced by keratinocytes and can inhibit detachment of corneocytes from human plantar callus in vitro, while a weaker KLK7 inhibitor, elafin (skin-derived antileukoprotease), can reduce the shedding of

corneocytes. Established epidermal mouse models overexpressing KLK7 have been shown to develop chronic itchy dermatitis. Further characterisation of these models also revealed epidermal hyperproliferation, decreased skin barrier function, and decreased expression of MHC II antigen in keratinocytes. These data provide an *in vivo* pathophysiological foundation that KLK7 plays an important role in skin, such as listed those below.

KLK cascade activation systems have been described. KLK7 is activated by KLK5 and KLK12. KLK7 activates other members of the kallikrein-related peptidase family including KLK1, KLK2, prostate specific antigen (PSA/KLK3) and KLK9.

The function of the putative N-terminal truncated KLK7 remains to be established.

Homology

At the protein level, KLK7 shares 28% (KLK12), 33% (KLK9), 36% (KLK10, 11), 37% (KLK1, KLK3/PSA), 38% (KLK2, KLK5, KLK6, KLK13), 40% (KLK8), 41% (KLK14), 43% (KLK4) and 42.6% (KLK15) sequence homology with other members of the kallikrein-related peptidase family.

Mutations

Germinal

An AACC insertion in the 3'UTR of the KLK7 gene has been found, which altered the common allele AACC to the rare allele AACCAACC. This insertion was found to be associated with atopic dermatitis.

Implicated in

Endocrine related cancers

Disease

It has been postulated that KLK7 plays a role in endocrine related cancers given its (a) dysregulated expression in cancerous tissues compared to normal tissues, (b) regulation by hormones, such as, oestradiol, progestins and glucocorticoids and (c) potential roles in degradation of cell-cell adhesion proteins, extracellular matrix (ECM) proteins and activation of other proteases and growth factors.

Epithelial ovarian carcinoma (EOC)

Disease

Kallikrein 7 is highly expressed in serous EOC at both the mRNA and protein levels, and high KLK7 mRNA expression is associated with poorly differentiated, late clinical stage ovarian carcinomas and the volume of residual tumour after surgery. Upregulated KLK7 protein was detected in EOC patient sera and tumour cytosols using ELISA, and in EOC tissue sections using immunohistochemistry and a quantitative automated *in situ* immuno-fluorescence-based protein analysis. At the mRNA level, both KLK7 and its exon

1 deleted short KLK7 transcripts were detected in serous EOC cells, while none or only KLK7 short transcript was found in normal ovarian epithelial cells. In addition, a coordinated expression pattern and co-localisation of KLK7 and KLK5 were found in serous EOC cells suggesting a proteolytic cascade between them. Co-overexpression of KLK4, KLK5, KLK6 and KLK7 in ovarian cancer cells (OV-MZ-6) led to increased invasion *in vitro* and resulted in increased tumour burden in nude mice. A coordinated expression of KLK7 and protease inhibitor antileukoprotease was also found in EOC cells. Of interest, the 110-139 amino acid region of the KLK7 protein incorporates multiple CD8⁺ CTL and CD4⁺ helper T cell epitopes, and represents an attractive target antigen for immunotherapy of ovarian cancer.

Prognosis

EOC patients with KLK7 mRNA or protein expression in their tumours had a significantly shorter disease-free survival time than those with KLK7 negative tumours. KLK7 is an independent unfavourable predictor of disease-free and overall survival for patients with low grade cancers. KLK7 has been shown to increase specificity for diagnosis and prognosis of EOC in conjunction with other biomarkers, such as CA125, HE4 and B7-H4.

Breast cancer

Disease

KLK7 gene expression was significantly lower in tumour tissues from early stage (I/II) breast cancer patients and tumour cells with progesterone receptors.

Prognosis

Two groups have reported conflicting data regarding the prognoses for breast cancer patients and KLK7 expressing tumours. One study found that breast cancer patients with KLK7 positive tumours have relatively shorter disease-free survival and overall survival than patients with KLK7 negative tumours. However, another study reported that breast cancer patients with KLK7 expressing tumours have favourable outcomes compared to those with KLK7 negative tumours.

Cervical cancer

Disease

In a study of 18 cervical cancer cell lines (10 primary and 8 established cell lines) and 8 normal cervical keratinocyte cell lines, KLK7 mRNA expression was detected in the cancer cells (5/10 primary and 4/8 established lines) but not in any of the normal cervical keratinocytes. Interestingly, all five patients, who harbour KLK7 positive tumours that were used to establish the primary cell lines, were found to have metastatic involvement of the pelvic tumour draining lymph nodes. In the same study, tumour restricted expression of KLK7 was confirmed by immunohistochemistry staining in 4 of the 5 primary

squamous cervical tumours, and 1 of the 4 primary adenocarcinomas, but none of the normal cervical epithelial cells. Another immuno-histochemical study showed a significantly higher expression of KLK7 in cervical adenocarcinomas compared to normal endocervical glands.

Pancreatic cancer

Disease

KLK7 is expressed in normal pancreas at mRNA and protein levels, and KLK7 protein is localised in acinar cells of the pancreas by immunohistochemical staining. KLK7 is overexpressed in pancreatic adenocarcinomas at both the mRNA and protein levels. KLK7 expression was also observed in neoplastic cells of all tumours examined using immunohistochemistry with moderate-to-intense staining in 16 of the 23 tumours examined. Only 2 of the 13 nonmalignant tissue specimens displayed moderate KLK7 staining, whereas the remaining specimens showed weak immunoreactivity. In pancreatic cancer cells, KLK7 was shown to i) cleave desmoglein 2, ii) cleave E-cadherin and the ECM protein, fibronectin, iii) enhance urokinase-type plasminogen activator receptor shedding, and iv) reduce cell aggregation and adhesion to vitronectin to promote pancreatic cancer invasion.

Oral squamous cell carcinoma (OSCC)

Disease

cDNA microarray analysis revealed that KLK5, KLK7, KLK8 and KLK10 were upregulated in tumour samples versus normal controls. RT-qPCR analysis confirmed that KLK7 mRNA was most differentially regulated with a 5.3-fold increase, while 2.8-, 4.0- and 3.5-fold increases were observed for KLK5, KLK8, and KLK10, respectively. Immunohistochemical analysis demonstrated strong reactivity for all 4 KLK proteins in both orthotopic murine tumours and human OSCC tissues.

Lung cancer

Disease

KLK7 mRNA levels are decreased in adenocarcinoma compared to matched nonmalignant lung tissue. Similarly, sera of patients with non-small cell lung cancer (NSCLC) have lower protein levels of KLK7, KLK5, KLK8, KLK10 and KLK12 than those from normal subjects. However, a study has reported intense cytoplasmic staining for KLK7, KLK5, KLK6 and KLK8 in 40-90% of squamous cell carcinomas, small cell carcinomas and carcinoid tumours while 20% of tumour cells had intense nuclear staining for KLK7, KLK5 and KLK8.

Brain tumours

Disease

RT-qPCR analysis showed that KLK7 mRNA expression in intracranial tumours was associated with shorter overall survival than those tumours with no

KLK7 expression from a survival analysis study of 73 patients with intracranial tumours. Overexpression of KLK7 protein by cultivated brain tumour cells significantly enhanced the invasive potential in a Matrigel invasion assay.

Colon cancer

Disease

One study using a semi-quantitative RT-PCR method showed that the KLK7 gene is up-regulated in colon cancer and its expression predicts poor prognosis for colon cancer patients.

Skin disorders

Note

A majority of studies have concentrated on the concomitant functions of KLK7 and KLK5 in normal human skin and a number of skin disorders given its (a) high expression in pathological conditions compared to normal skin samples, (b) cleavage/degradation of intercellular adhesive glycoproteins and (c) potential of activation and degradation of cytokines, such as interleukin 1beta (IL-1b).

Netherton syndrome (NS)

Disease

NS is a rare but severe inherited disorder that presents the three following characteristics with varying degrees of severity of their symptoms. 1) Ichthyosiform erythroderma - inflamed, red, scaly skin and trichorrhexis invaginata ("bamboo hair"). 2) Short, brittle, lustreless hair and atopic diathesis. 3) Predisposition to allergy problems.

NS patients have mutations in the serine protease inhibitor Kazal-type 5 (SPINK5) gene, encoding the protease inhibitor LEKTI (lympho-epithelial Kazal-type related inhibitor). Early studies using mouse models revealed that SPINK5-deficient mice mimic NS through degradation of desmoglein 1 by epidermal protease. The pathophysiological processes in the skin and epithelial related tissues of NS patients result from the lack of functional LEKTI protease inhibitor and consequently the over-degradation of corneodesmosomal cadherins by KLK7, KLK5 and KLK14.

The SPINK5 gene is localised chromosome 5. SPINK5 mutations introduce premature termination codons in LEKTI transcripts and lead to the production of truncated LEKTI forms that lack several inhibitory domains. NS is an autosomal recessive condition.

Atopic dermatitis (AD)

Disease

AD is a chronic inflammatory and allergic skin disorder. Multifactorial studies have suggested that both genetic and environmental factors contribute to AD development. A study comprising 103 AD patients

and 261 matched controls revealed a significant association between the rare AACCAACC allele in the 3'UTR of KLK7 with AD. However, another group found that the AACCAACC allele was not associated with AD in a cohort of 99 patients and 189 controls. Nevertheless, patients with the AACCAACC allele have increased KLK7 protease activity resulting in premature breakdown of corneodesmosomes, and leading to impairment of the epidermal barrier. Furthermore, acute eczematous lesions and clinically unaffected skin can further increase production of KLK7 and epidermal barrier functions are damaged through environmental interactions, such as washing with soap and detergents, or long-term application of corticosteroids. A combination of the above factors leads to a defective skin barrier and increases the risk of allergen penetration and succeeding inflammatory reaction. By ELISA, KLK7 levels were found to be elevated in the stratum corneum of AD patients, and KLK7 in the serum significantly correlated with eosinophil counts in the blood of AD patients, indicative of the body under an allergic condition.

Psoriasis

Disease

A number of early studies reported that the chymotrypsin-like activity in stratum corneum was slightly elevated in psoriasis, but KLK7 serum levels did not differ between normal volunteers and patients with psoriasis. It has been confirmed that KLK7 protein levels were similar between non-lesional and lesional skin extracts, but increased amounts of desmoglein 1, plakoglobin and high molecular weight fragments of desmocollin 1 were detected in the lesional skin, suggesting an involvement of other proteases.

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